

sent
STIC-Biotech/ChemLib

184456

From: Chan, Christina
Sent: Thursday, April 06, 2006 10:44 AM
To: Steadman, David (AU1652); STIC-Biotech/ChemLib
Subject: RE: RUSH sequence search request for 09/806,413

~~Please rush. Thanks Chris~~

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

CRFC

-----Original Message-----

From: Steadman, David (AU1652)
Sent: Thursday, April 06, 2006 8:02 AM
To: Chan, Christina
Subject: RUSH sequence search request for 09/806,413

Ms. Chan,

An after-final amendment has been filed in 09/806,413 and the claim appears to be in condition for allowance. I would like to request a RUSH sequence search. SEQ ID NO:8 is 466 amino acids. Thank you -

David

NAME: David Steadman
AU: 1656
Date: 4/6/06
Office: Remsen 2B05
Mailbox: Remsen 3C70

Please perform the following searches in commercial and interference databases:

- 1) Standard search of SEQ ID NO:8 against amino acid databases.
- 2) Standard search of SEQ ID NO:8 against nucleic acid databases.

Please save results to diskette.

Thank you very much.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

GenCore version 5.1.7

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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:33:45 ; Search time 188 Seconds
 (without alignments)
 1089.098 Million cell updates/sec

Title: US-09-806-413A-8
 Perfect score: 2490
 Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLPSA 466

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:*
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*
 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	2490	100.0	466	3 AAY82580	Aay82580 Aspergill
2	2490	100.0	488	3 AAY82581	Aay82581 Aspergill
3	1877	75.4	490	4 AAB73383	Aab73383 Trichoder
4	1440.5	57.9	426	8 ADN20583	Adn20583 Bacterial
5	1189.5	47.8	452	4 AAB73382	Aab73382 Trichoder
6	517	20.8	469	8 ADS27884	Ads27884 Bacterial
7	397	15.9	508	8 ADN23340	Adn23340 Bacterial
8	386	15.5	561	8 ADN22686	Adn22686 Bacterial
9	358.5	14.4	515	7 ADB79844	Adb79844 Mouse put
10	340.5	13.7	566	8 ADN22685	Adn22685 Bacterial
11	333	13.4	497	4 AAU05669	Aau05669 Human glu
12	332	13.3	497	4 AAU05670	Aau05670 Human glu
13	331	13.3	497	4 AAU05667	Aau05667 Human glu

14	331	13.3	497	4	AAU05685	Aau05685	Human	glu
15	329	13.2	497	4	AAU05668	Aau05668	Human	glu
16	329	13.2	497	4	AAU05673	Aau05673	Human	glu
17	329	13.2	497	4	AAU05659	Aau05659	Human	glu
18	329	13.2	497	4	AAU05684	Aau05684	Human	glu
19	329	13.2	516	1	AAP81987	Aap81987	Recombina	
20	328	13.2	497	4	AAU05660	Aau05660	Human	glu
21	328	13.2	497	4	AAU05686	Aau05686	Human	glu
22	328	13.2	497	8	ADT98123	Adt98123	Human	glu
23	328	13.2	497	8	ADT98128	Adt98128	Human	glu
24	328	13.2	497	8	ADT98136	Adt98136	Human	glu
25	328	13.2	497	8	ADT98130	Adt98130	Human	glu
26	328	13.2	497	8	ADT98135	Adt98135	Human	glu
27	328	13.2	497	8	ADT98129	Adt98129	Human	glu
28	327	13.1	497	4	AAU05691	Aau05691	Human	glu
29	327	13.1	497	4	AAU05690	Aau05690	Human	glu
30	327	13.1	497	4	AAU05695	Aau05695	Human	glu
31	327	13.1	497	8	ADT98133	Adt98133	Human	glu
32	327	13.1	497	8	ADT98132	Adt98132	Human	glu
33	327	13.1	497	8	ADT98126	Adt98126	Human	glu
34	327	13.1	497	8	ADT98125	Adt98125	Human	glu
35	327	13.1	536	4	AAB61496	Aab61496	protein e	
36	327	13.1	536	4	AAB61495	Aab61495	Protein e	
37	326	13.1	497	4	AAU05655	Aau05655	Human	glu
38	326	13.1	497	4	AAU05699	Aau05699	Human	glu
39	325	13.1	497	4	AAU05692	Aau05692	Human	glu
40	324	13.0	497	4	AAU05675	Aau05675	Human	glu
41	324	13.0	497	4	AAU05662	Aau05662	Human	glu
42	324	13.0	497	4	AAU05687	Aau05687	Human	glu
43	324	13.0	497	4	AAU05656	Aau05656	Human	glu
44	324	13.0	497	4	AAU05694	Aau05694	Human	glu
45	323	13.0	497	4	AAU05696	Aau05696	Human	Mat

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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:41:29 ; Search time 48 Seconds
 (without alignments)
 802.643 Million cell updates/sec

Title: US-09-806-413A-8
 Perfect score: 2490
 Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLPSA 466

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	327	13.1	536	2	US-09-586-216C-12	Sequence 12, Appl
2	327	13.1	536	2	US-09-586-216C-14	Sequence 14, Appl
3	323	13.0	497	2	US-10-360-101-201	Sequence 201, App
4	323	13.0	497	2	US-10-360-101-244	Sequence 244, App
5	323	13.0	498	1	US-08-080-855-1	Sequence 1, Appli
6	323	13.0	516	2	US-09-715-858-6	Sequence 6, Appli
7	323	13.0	536	2	US-09-715-858-8	Sequence 8, Appli
8	323	13.0	536	2	US-09-538-092-841	Sequence 841, App
9	323	13.0	569	2	US-09-949-016-11329	Sequence 11329, A
10	322	12.9	546	1	US-08-713-928B-4	Sequence 4, Appli
11	217	8.7	465	2	US-09-658-772-2	Sequence 2, Appli
12	217	8.7	465	2	US-10-159-487-2	Sequence 2, Appli
13	147	5.9	819	2	US-09-328-352-4650	Sequence 4650, Ap
14	134.5	5.4	669	2	US-09-949-016-5895	Sequence 5895, Ap
15	134.5	5.4	669	2	US-09-949-016-7367	Sequence 7367, Ap
16	132.5	5.3	3892	2	US-09-328-352-5503	Sequence 5503, Ap

17	121	4.9	1026	1	US-08-194-290-7	Sequence 7, Appli
18	121	4.9	1026	1	US-08-614-377A-7	Sequence 7, Appli
19	121	4.9	1026	2	US-09-142-648B-7	Sequence 7, Appli
20	119	4.8	673	2	US-09-107-532A-5134	Sequence 5134, Ap
21	118.5	4.8	827	2	US-09-543-681A-6425	Sequence 6425, Ap
22	118	4.7	1216	2	US-09-134-000C-5130	Sequence 5130, Ap
23	117.5	4.7	422	1	US-08-712-072C-2	Sequence 2, Appli
24	117.5	4.7	1032	2	US-09-733-643B-16	Sequence 16, Appl
25	117	4.7	335	2	US-09-570-856B-15	Sequence 15, Appl
26	117	4.7	343	2	US-10-148-306-21	Sequence 21, Appl
27	116.5	4.7	330	2	US-10-104-047-1985	Sequence 1985, Ap
28	116	4.7	1391	2	US-10-080-505-15	Sequence 15, Appl
29	115.5	4.6	1016	2	US-10-197-220-95	Sequence 95, Appl
30	115	4.6	558	2	US-10-104-047-2054	Sequence 2054, Ap
31	114	4.6	365	2	US-09-902-540-10979	Sequence 10979, A
32	114	4.6	872	1	US-08-387-942C-5	Sequence 5, Appli
33	114	4.6	1391	2	US-10-080-505-11	Sequence 11, Appl
34	113.5	4.6	700	1	US-07-862-588B-2	Sequence 2, Appli
35	113	4.5	997	1	US-08-387-942C-4	Sequence 4, Appli
36	112	4.5	655	1	US-08-469-202-28	Sequence 28, Appl
37	112	4.5	655	1	US-08-484-434C-35	Sequence 35, Appl
38	112	4.5	655	2	US-09-384-361-35	Sequence 35, Appl
39	111.5	4.5	750	6	5457037-3	Patent No. 5457037
40	111.5	4.5	751	6	5457037-5	Patent No. 5457037
41	111.5	4.5	776	2	US-09-346-237-7	Sequence 7, Appli
42	111.5	4.5	1767	2	US-09-583-110-3975	Sequence 3975, Ap
43	111.5	4.5	1769	2	US-09-107-433-3676	Sequence 3676, Ap
44	111	4.5	655	1	US-08-469-202-27	Sequence 27, Appl
45	111	4.5	655	1	US-08-484-434C-34	Sequence 34, Appl

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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:52:43 ; Search time 169 Seconds
 (without alignments)
 1152.121 Million cell updates/sec

Title: US-09-806-413A-8
 Perfect score: 2490
 Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLPSA 466

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_Main:*
 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1440.5	57.9	426	4	US-10-369-493-3236	Sequence 3236, Ap
2	550	22.1	647	4	US-10-156-761-10246	Sequence 10246, A
3	517	20.8	469	4	US-10-369-493-16917	Sequence 16917, A
4	397	15.9	508	4	US-10-369-493-5993	Sequence 5993, Ap
5	386	15.5	561	4	US-10-369-493-5339	Sequence 5339, Ap
6	358.5	14.4	515	4	US-10-205-219-84	Sequence 84, Appl
7	340.5	13.7	566	4	US-10-369-493-5338	Sequence 5338, Ap
8	327	13.1	516	5	US-10-988-428-1	Sequence 1, Appli
9	327	13.1	516	5	US-10-988-427-1	Sequence 1, Appli
10	327	13.1	536	4	US-10-706-466-12	Sequence 12, Appl
11	327	13.1	536	4	US-10-706-466-14	Sequence 14, Appl
12	323	13.0	497	3	US-09-753-126-1	Sequence 1, Appli
13	323	13.0	497	3	US-09-896-896A-1	Sequence 1, Appli
14	323	13.0	497	4	US-10-330-697-1	Sequence 1, Appli
15	323	13.0	497	4	US-10-360-101-201	Sequence 201, App
16	323	13.0	497	4	US-10-360-101-244	Sequence 244, App

17	323	13.0	497	5	US-10-784-295-8	Sequence 8, Appli
18	323	13.0	516	4	US-10-240-687-2	Sequence 2, Appli
19	323	13.0	516	4	US-10-240-687-4	Sequence 4, Appli
20	323	13.0	516	4	US-10-421-175-6	Sequence 6, Appli
21	323	13.0	526	5	US-10-784-295-14	Sequence 14, Appl
22	323	13.0	536	4	US-10-024-197-25	Sequence 25, Appl
23	323	13.0	536	4	US-10-024-197-26	Sequence 26, Appl
24	323	13.0	536	4	US-10-421-175-8	Sequence 8, Appli
25	323	13.0	536	4	US-10-411-037-24	Sequence 24, Appl
26	323	13.0	536	4	US-10-411-026-24	Sequence 24, Appl
27	323	13.0	536	4	US-10-410-962-24	Sequence 24, Appl
28	323	13.0	536	4	US-10-411-049-24	Sequence 24, Appl
29	323	13.0	536	4	US-10-410-930-24	Sequence 24, Appl
30	323	13.0	536	4	US-10-410-997-24	Sequence 24, Appl
31	323	13.0	536	4	US-10-411-012-24	Sequence 24, Appl
32	323	13.0	536	4	US-10-287-994-24	Sequence 24, Appl
33	323	13.0	536	4	US-10-410-913-24	Sequence 24, Appl
34	323	13.0	536	5	US-10-410-980-24	Sequence 24, Appl
35	323	13.0	536	5	US-10-410-897-24	Sequence 24, Appl
36	323	13.0	536	5	US-10-492-261-24	Sequence 24, Appl
37	323	13.0	592	3	US-09-753-126-4	Sequence 4, Appli
38	323	13.0	592	4	US-10-330-697-4	Sequence 4, Appli
39	318	12.8	416	4	US-10-369-493-15956	Sequence 15956, A
40	318	12.8	416	4	US-10-369-493-16319	Sequence 16319, A
41	318	12.8	420	4	US-10-369-493-15580	Sequence 15580, A
42	312	12.5	514	4	US-10-466-593-1	Sequence 1, Appli
43	289	11.6	522	4	US-10-369-493-6240	Sequence 6240, Ap
44	289	11.6	522	4	US-10-369-493-6241	Sequence 6241, Ap
45	251.5	10.1	1567	6	US-11-097-143-21768	Sequence 21768, A

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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:53:43 ; Search time 25 Seconds
 (without alignments)
 581.419 Million cell updates/sec

Title: US-09-806-413A-8
 Perfect score: 2490
 Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLPSA 466

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 184161 seqs, 31191982 residues

Total number of hits satisfying chosen parameters: 184161

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published_Applications_AA_New:*
 1: /SIDS5/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
 3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 4: /SIDS5/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 5: /SIDS5/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 6: /SIDS5/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 7: /SIDS5/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
 8: /SIDS5/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	323	13.0	516	6	US-10-506-448A-2	Sequence 2, Appli
2	323	13.0	536	7	US-11-183-205-24	Sequence 24, Appl
3	222.5	8.9	463	6	US-10-517-939-314	Sequence 314, App
4	205	8.2	422	6	US-10-517-939-238	Sequence 238, App
5	197.5	7.9	426	6	US-10-517-939-240	Sequence 240, App
6	187.5	7.5	423	6	US-10-517-939-244	Sequence 244, App
7	183	7.3	564	6	US-10-517-939-242	Sequence 242, App
8	176.5	7.1	512	6	US-10-517-939-236	Sequence 236, App
9	157.5	6.3	401	6	US-10-517-939-246	Sequence 246, App
10	132.5	5.3	5291	7	US-11-052-554A-281	Sequence 281, App
11	124	5.0	335	6	US-10-517-939-232	Sequence 232, App
12	120	4.8	7465	7	US-11-087-099-7521	Sequence 7521, Ap
13	119	4.8	1461	7	US-11-052-554A-283	Sequence 283, App
14	116.5	4.7	330	7	US-11-072-512-1985	Sequence 1985, Ap

15	116.5	4.7	1256	6	US-10-493-909-90	Sequence 90, Appl
16	116	4.7	3132	7	US-11-087-099-1245	Sequence 1245, Ap
17	115.5	4.6	1016	7	US-11-103-957-41	Sequence 41, Appl
18	115.5	4.6	1016	7	US-11-018-868-22	Sequence 22, Appl
19	115	4.6	281	6	US-10-204-639-28	Sequence 28, Appl
20	115	4.6	558	7	US-11-072-512-2054	Sequence 2054, Ap
21	115	4.6	3300	7	US-11-052-554A-133	Sequence 133, App
22	114	4.6	549	7	US-11-085-185-2	Sequence 2, Appli
23	111.5	4.5	1767	7	US-11-052-554A-372	Sequence 372, App
24	111.5	4.5	1767	7	US-11-089-508-4	Sequence 4, Appli
25	109.5	4.4	710	7	US-11-089-551A-33	Sequence 33, Appl
26	108.5	4.4	1007	6	US-10-517-939-84	Sequence 84, Appl
27	107.5	4.3	1324	7	US-11-089-508-12	Sequence 12, Appl
28	107	4.3	176	7	US-11-096-568A-19161	Sequence 19161, A
29	106.5	4.3	2902	7	US-11-052-554A-91	Sequence 91, Appl
30	106	4.3	1643	7	US-11-052-554A-172	Sequence 172, App
31	105.5	4.2	3194	7	US-11-052-554A-90	Sequence 90, Appl
32	104	4.2	866	7	US-11-052-554A-29	Sequence 29, Appl
33	104	4.2	2399	7	US-11-052-554A-92	Sequence 92, Appl
34	103	4.1	611	6	US-10-517-939-156	Sequence 156, App
35	102.5	4.1	354	6	US-10-517-939-216	Sequence 216, App
36	102.5	4.1	413	7	US-11-087-099-3343	Sequence 3343, Ap
37	102.5	4.1	834	7	US-11-052-554A-212	Sequence 212, App
38	102.5	4.1	2204	7	US-11-052-554A-134	Sequence 134, App
39	102	4.1	444	7	US-11-074-176-170	Sequence 170, App
40	102	4.1	613	6	US-10-517-939-298	Sequence 298, App
41	101.5	4.1	2333	6	US-10-453-372-170	Sequence 170, App
42	101.5	4.1	2662	6	US-10-453-372-114	Sequence 114, App
43	101.5	4.1	2724	6	US-10-453-372-148	Sequence 148, App
44	101.5	4.1	2733	6	US-10-453-372-136	Sequence 136, App
45	101.5	4.1	2733	6	US-10-453-372-142	Sequence 142, App

GenCore version 5.1.7

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2006, 12:24:52 ; Search time 5951 Seconds
(without alignments)
4451.193 Million cell updates/sec

Title: US-09-806-413A-8
Perfect score: 2490
Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLP SA 466

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US09806413/runat_07042006_132430_29776/app_query.fasta_1
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p
-USER=US09806413@CGN_1_1_7415@runat_07042006_132430_29776 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query		SUMMARIES				Description
No.	Score	Match Length	DB	ID			
1	1877	75.4	1696	15	THA243823		AJ243823 Trichoder
2	1555.5	62.5	1510	15	AB073820		AB073820 Neurospor
c 3	1544.5	62.0	197698	15	BX908809		BX908809 Neurospor
4	1233.5	49.5	1528	15	THA243807		AJ243807 Trichoder
5	550	22.1	110000	1	BA000030_33		Continuation (34 o
6	517	20.8	14878	1	AE005849		AE005849 Caulobact
7	493.5	19.8	304230	1	AE016940		AE016940 Bacteroid
8	406	16.3	1891	2	AK114510		AK114510 Ciona int
9	401.5	16.1	9661	1	AE013177		AE013177 Thermoana
10	359.5	14.4	1684	6	AX683111		AX683111 Sequence
11	359.5	14.4	1684	9	MUSGCB		M24119 Mouse gluco
12	359.5	14.4	1964	9	BC006663		BC006663 Mus muscu
13	349.5	14.0	35129	15	AC151930		AC151930 Phaeodact
c 14	346	13.9	110000	1	CP000050_37		Continuation (38 o
c 15	346	13.9	110000	1	CP000050_38		Continuation (39 o
16	336	13.5	11594	1	AE012205		AE012205 Xanthomon
17	329.5	13.2	10007	1	AE011746		AE011746 Xanthomon
18	327	13.1	1551	6	AX191972		AX191972 Sequence
19	327	13.1	1551	6	AX349364		AX349364 Sequence
20	327	13.1	1741	6	AR477243		AR477243 Sequence
21	327	13.1	1741	6	AR477244		AR477244 Sequence
22	327	13.1	1792	8	HUMGCB		K02920 Homo sapien
23	326	13.1	1661	6	I09351		I09351 Sequence 1
24	323	13.0	1551	6	AR344266		AR344266 Sequence
25	323	13.0	1551	6	AX147656		AX147656 Sequence
26	323	13.0	1551	6	AX840227		AX840227 Sequence
27	323	13.0	1592	6	AX299777		AX299777 Sequence
28	323	13.0	1593	6	AX299779		AX299779 Sequence
29	323	13.0	1611	6	AR344267		AR344267 Sequence
30	323	13.0	1611	6	AX147658		AX147658 Sequence
31	323	13.0	1611	11	AY891754		AY891754 Synthetic
32	323	13.0	1611	11	AY891755		AY891755 Synthetic
33	323	13.0	1611	11	BT008212		BT008212 Synthetic
34	323	13.0	2259	8	HUMGCA		D13286 Homo sapien
35	323	13.0	2275	6	CQ882045		CQ882045 Sequence
36	323	13.0	2275	8	HUMGCBPRC		M19285 Human gluco
37	323	13.0	2279	8	BC003356		BC003356 Homo sapi
38	323	13.0	2408	8	HSM808635		BX648487 Homo sapi
39	323	13.0	2586	6	AX752903		AX752903 Sequence
40	323	13.0	2587	8	HUMGCB		M16328 Human gluco
41	321	12.9	1344	1	AF231759		AF231759 Salmonell
42	321	12.9	20029	1	AE008907		AE008907 Salmonell
43	320	12.9	2277	6	CQ715240		CQ715240 Sequence
44	318.5	12.8	1949	15	AF352032		AF352032 Phytophth
c 45	312.5	12.6	110000	1	CP000083_38		Continuation (39 o

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2006, 12:25:05 ; Search time 863 Seconds
 (without alignments)
 3598.780 Million cell updates/sec

Title: US-09-806-413A-8
 Perfect score: 2490
 Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLPSA 466

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
 -Q=/abss/ABSSWEB_spool/US09806413/runat_07042006_132429_29764/app_query.fasta_1
 -DB=N_Geneseq -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss03h
 -USER=US09806413@CGN_1_1_727@runat_07042006_132429_29764 -NCPU=6 -ICPU=3
 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_21:*
 1: geneseqn1980s:*
 2: geneseqn1990s:*
 3: geneseqn2000s:*
 4: geneseqn2001as:*
 5: geneseqn2001bs:*
 6: geneseqn2002as:*
 7: geneseqn2002bs:*
 8: geneseqn2003as:*
 9: geneseqn2003bs:*
 10: geneseqn2003cs:*
 11: geneseqn2003ds:*
 12: geneseqn2004as:*
 13: geneseqn2004bs:*
 14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2490	100.0	1401	3	AAA13840	Aaa13840 Aspergill
2	2490	100.0	1647	3	AAA13841	Aaa13841 Aspergill
3	1877	75.4	1696	4	AAF76269	Aaf76269 Trichoder
4	1440.5	57.9	1278	13	ADS48493	Ads48493 Bacterial
5	1233.5	49.5	1528	4	AAF76268	Aaf76268 Trichoder
6	517	20.8	1410	13	ADT42166	Adt42166 Bacterial
7	359.5	14.4	1684	10	ADB79845	Adb79845 Mouse put
8	329	13.2	1661	1	AAN80113	Aan80113 Encodes r
9	327	13.1	1551	4	AAS10863	Aas10863 Human cDN
10	327	13.1	1551	6	ABK40235	Abk40235 DNA encod
11	327	13.1	1741	4	AAF28294	Aaf28294 Modified
12	327	13.1	1741	4	AAF28293	Aaf28293 Unmodifie
13	327	13.1	1792	6	ABS69894	Abs69894 Human lys
14	323	13.0	1491	14	ADU63872	Adu63872 Human glu
15	323	13.0	1551	4	AAD06388	Aad06388 Human glu
16	323	13.0	1551	10	ACF80575	Acf80575 Human glu
17	323	13.0	1592	6	AAH99924	Aah99924 Nucleotid
18	323	13.0	1593	6	AAH99925	Aah99925 Nucleotid
19	323	13.0	1611	4	AAD06389	Aad06389 Human glu
20	323	13.0	1661	2	AAX26682	Aax26682 Complete
21	323	13.0	1661	3	AAA48444	Aaa48444 Human lys
22	323	13.0	2004	10	ACC78880	Acc78880 Human glu
23	323	13.0	2004	12	ADN49695	Adn49695 Human glu
24	323	13.0	2004	13	ADU74371	Adu74371 Human glu
25	323	13.0	2186	14	ADU63878	Adu63878 Recombina
26	323	13.0	2275	12	ADN04372	Adn04372 Antipsori
27	323	13.0	2275	13	ADP24196	Adp24196 PRO polyp
28	323	13.0	2275	13	ADS19469	Ads19469 Beta-gluc
29	323	13.0	2275	14	AEB34810	Aeb34810 DNA encod
30	323	13.0	2279	9	ADA37283	Ada37283 Acid beta
31	323	13.0	2576	11	ACN90350	Acn90350 Breast ca
32	323	13.0	2586	10	ADE76203	Ade76203 Human glu
33	322	12.9	1264	13	ADS63593	Ads63593 Bacterial
34	322	12.9	1642	2	AAT71753	Aat71753 Human glu
35	318	12.8	1248	13	ADT41568	Adt41568 Bacterial
36	318	12.8	1248	13	ADS63969	Ads63969 Bacterial
37	315	12.7	2521	12	ADQ83233	Adq83233 Human tum
38	315	12.7	2521	12	ADQ85144	Adq85144 Human tum
39	315	12.7	2521	13	ADQ83913	Adq83913 Human tum
40	305	12.2	3307	11	ADI30980	Adi30980 Human cDN
41	305	12.2	3307	13	ADS83047	Ads83047 Human lym
42	290.5	11.7	1314	10	ACF68125	Acf68125 Photorhab
c 43	290.5	11.7	110000	10	ACF67367_08	Continuation (9 of
c 44	290.5	11.7	110000	10	ACF65384_2	Continuation (3 of
45	264.5	10.6	2294	13	ACN42233	Acn42233 Human dia

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2006, 12:24:48 ; Search time 262 Seconds
 (without alignments)
 3161.617 Million cell updates/sec

Title: US-09-806-413A-8
 Perfect score: 2490
 Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLP SA 466

Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
 -Q=/abss/ABSSWEB_spool/US09806413/runat_07042006_132434_29864/app_query.fasta_1
 -DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
 -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -HOST=abss07 -USER=US09806413 @CGN_1_1_193 @runat_07042006_132434_29864
 -NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
 1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
 2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
 5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
 6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
 8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
 9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%
 Result Query

No.	Score	Match	Length	DB	ID	Description
1	327	13.1	1741	3	US-09-586-216C-11	Sequence 11, Appl
2	327	13.1	1741	3	US-09-586-216C-13	Sequence 13, Appl
3	327	13.1	1792	3	US-09-782-378A-16	Sequence 16, Appl
4	323	13.0	1551	3	US-09-715-858-5	Sequence 5, Appli
5	323	13.0	1611	3	US-09-715-858-7	Sequence 7, Appli
6	323	13.0	2294	3	US-09-949-016-5458	Sequence 5458, Ap
7	322	12.9	1642	2	US-08-713-928B-3	Sequence 3, Appli
8	305	12.2	3307	3	US-09-023-655-306	Sequence 306, App
9	217	8.7	1518	3	US-09-658-772-1	Sequence 1, Appli
10	217	8.7	1518	3	US-10-159-487-1	Sequence 1, Appli
11	149	6.0	2711	3	US-10-104-047-15	Sequence 15, Appl
12	147	5.9	2460	3	US-09-328-352-524	Sequence 524, App
c 13	140.5	5.6	10733	3	US-09-902-540-1021	Sequence 1021, Ap
14	140.5	5.6	25165	3	US-09-453-702B-39	Sequence 39, Appl
15	140.5	5.6	25165	3	US-10-114-170-39	Sequence 39, Appl
16	136.5	5.5	3986	3	US-09-949-016-24	Sequence 24, Appl
17	134.5	5.4	3257	3	US-09-949-016-1496	Sequence 1496, Ap
18	132.5	5.3	1479	3	US-09-533-559-7463	Sequence 7463, Ap
19	132.5	5.3	11679	3	US-09-328-352-1377	Sequence 1377, Ap
20	126.5	5.1	1408	2	US-08-712-072C-1	Sequence 1, Appli
21	125.5	5.0	1722	3	US-09-252-991A-14763	Sequence 14763, A
22	122.5	4.9	1473	2	US-08-672-571A-2	Sequence 2, Appli
23	121	4.9	3300	2	US-08-194-290-6	Sequence 6, Appli
24	121	4.9	3300	2	US-08-614-377A-6	Sequence 6, Appli
25	121	4.9	3300	3	US-09-142-648B-6	Sequence 6, Appli
26	120	4.8	1386	2	US-08-672-571A-4	Sequence 4, Appli
27	119	4.8	2022	3	US-09-107-532A-1480	Sequence 1480, Ap
c 28	119	4.8	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c 29	119	4.8	4411529	3	US-09-103-840A-1	Sequence 1, Appli
30	118.5	4.8	2484	3	US-09-543-681A-2253	Sequence 2253, Ap
31	118	4.7	3651	3	US-09-134-000C-1725	Sequence 1725, Ap
32	117.5	4.7	1854	3	US-09-894-844-103	Sequence 103, App
33	117.5	4.7	4411529	3	US-09-103-840A-1	Sequence 1, Appli
34	116	4.7	4822	3	US-10-080-505-14	Sequence 14, Appl
35	115.5	4.6	3048	3	US-10-197-220-80	Sequence 80, Appl
36	115	4.6	1176	3	US-09-902-540-3670	Sequence 3670, Ap
37	115	4.6	1934	3	US-09-799-451-938	Sequence 938, App
38	115	4.6	2087	3	US-10-104-047-84	Sequence 84, Appl
39	114.5	4.6	2625	9	5457037-4	Patent No. 5457037
40	114	4.6	1242	3	US-09-902-540-6322	Sequence 6322, Ap
c 41	114	4.6	1245	3	US-09-902-540-391	Sequence 391, App
42	114	4.6	1855	3	US-09-403-752A-86	Sequence 86, Appl
43	114	4.6	1855	3	US-09-551-151A-86	Sequence 86, Appl
44	114	4.6	4605	3	US-10-080-505-10	Sequence 10, Appl
45	114	4.6	12588	2	US-08-387-942C-1	Sequence 1, Appli

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2006, 12:25:08 ; Search time 1111 Seconds
(without alignments)
3468.524 Million cell updates/sec

Title: US-09-806-413A-8
Perfect score: 2490
Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLP SA 466

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09806413/runat_07042006_132440_24/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss05h
-USER=US09806413@CGN_1_1_1026@runat_07042006_132440_24 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1440.5	57.9	1278	6	US-10-369-493-26923	Sequence 26923, A	
2	550	22.1	1941	6	US-10-156-761-2696	Sequence 2696, Ap	
3	550	22.1	9025608	6	US-10-156-761-1	Sequence 1, Appli	
4	517	20.8	1410	6	US-10-369-493-40604	Sequence 40604, A	
5	359.5	14.4	1684	6	US-10-205-219-85	Sequence 85, Appl	
6	327	13.1	1551	3	US-09-753-126-2	Sequence 2, Appli	
7	327	13.1	1551	3	US-09-896-896A-2	Sequence 2, Appli	
8	327	13.1	1551	6	US-10-330-697-2	Sequence 2, Appli	
9	327	13.1	1741	7	US-10-706-466-11	Sequence 11, Appl	
10	327	13.1	1741	7	US-10-706-466-13	Sequence 13, Appl	
11	327	13.1	1792	3	US-09-782-378A-16	Sequence 16, Appl	
12	327	13.1	1792	9	US-10-988-428-2	Sequence 2, Appli	
13	327	13.1	1792	9	US-10-988-427-2	Sequence 2, Appli	
14	323	13.0	1491	8	US-10-784-295-7	Sequence 7, Appli	
15	323	13.0	1551	6	US-10-421-175-5	Sequence 5, Appli	
16	323	13.0	1592	6	US-10-240-687-1	Sequence 1, Appli	
17	323	13.0	1593	6	US-10-240-687-3	Sequence 3, Appli	
18	323	13.0	1611	6	US-10-421-175-7	Sequence 7, Appli	
19	323	13.0	2004	7	US-10-411-037-23	Sequence 23, Appl	
20	323	13.0	2004	7	US-10-411-026-23	Sequence 23, Appl	
21	323	13.0	2004	7	US-10-410-962-23	Sequence 23, Appl	
22	323	13.0	2004	7	US-10-411-049-23	Sequence 23, Appl	
23	323	13.0	2004	7	US-10-410-930-23	Sequence 23, Appl	
24	323	13.0	2004	7	US-10-410-997-23	Sequence 23, Appl	
25	323	13.0	2004	7	US-10-411-012-23	Sequence 23, Appl	
26	323	13.0	2004	7	US-10-287-994-23	Sequence 23, Appl	
27	323	13.0	2004	7	US-10-410-913-23	Sequence 23, Appl	
28	323	13.0	2004	8	US-10-410-980-23	Sequence 23, Appl	
29	323	13.0	2004	9	US-10-410-897-23	Sequence 23, Appl	
30	323	13.0	2004	9	US-10-492-261-23	Sequence 23, Appl	
31	323	13.0	2186	8	US-10-784-295-13	Sequence 13, Appl	
32	323	13.0	2275	9	US-10-804-763-37	Sequence 37, Appl	
33	323	13.0	2275	10	US-11-036-643-12	Sequence 12, Appl	
34	323	13.0	2279	6	US-10-024-197-24	Sequence 24, Appl	
35	323	13.0	2576	5	US-10-198-846-11500	Sequence 11500, A	
36	323	13.0	2586	8	US-10-278-698-359	Sequence 359, App	
37	323	13.0	2586	8	US-10-278-698-873	Sequence 873, App	
38	323	13.0	2587	8	US-10-278-698-164	Sequence 164, App	
39	323	13.0	2587	8	US-10-278-698-680	Sequence 680, App	
40	322	12.9	1264	6	US-10-369-493-39267	Sequence 39267, A	
41	318	12.8	1248	6	US-10-369-493-39643	Sequence 39643, A	
42	318	12.8	1248	6	US-10-369-493-40006	Sequence 40006, A	
43	305	12.2	3307	7	US-10-641-643-306	Sequence 306, App	
44	255	10.2	4861	10	US-11-097-143-21767	Sequence 21767, A	
45	250	10.0	9517	10	US-11-097-143-21766	Sequence 21766, A	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2006, 12:25:21 ; Search time 4920 Seconds
(without alignments)
378.914 Million cell updates/sec

Title: US-09-806-413A-8
Perfect score: 2490
Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLP SA 466

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 9267905 seqs, 2000278028 residues

Total number of hits satisfying chosen parameters: 18535810

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US09806413/runat_07042006_132442_86/app_query.fasta_1
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss06p
-USER=US09806413@CGN_1_1_987_@runat_07042006_132442_86 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/1/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/1/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/1/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	327	13.1	1792	14	US-11-127-832-16	Sequence 16, Appl
2	323	13.0	1551	9	US-10-506-448A-1	Sequence 1, Appli
3	323	13.0	2004	11	US-11-183-205-23	Sequence 23, Appl
4	222.5	8.9	1392	8	US-10-517-939-313	Sequence 313, App
5	205	8.2	1269	8	US-10-517-939-237	Sequence 237, App
6	197.5	7.9	1281	8	US-10-517-939-239	Sequence 239, App
7	187.5	7.5	1272	8	US-10-517-939-243	Sequence 243, App
8	183	7.3	1695	8	US-10-517-939-241	Sequence 241, App
9	182	7.3	1263	8	US-10-517-939-245	Sequence 245, App
10	176.5	7.1	1539	8	US-10-517-939-235	Sequence 235, App
11	149	6.0	2711	11	US-11-072-512-15	Sequence 15, Appl
12	140.5	5.6	15876	14	US-11-052-554A-660	Sequence 660, App
13	136.5	5.5	3777	14	US-11-122-329-12	Sequence 12, Appl
14	126	5.1	1008	8	US-10-517-939-231	Sequence 231, App
15	119	4.8	4386	14	US-11-052-554A-662	Sequence 662, App
16	119	4.8	6615	14	US-11-052-554A-518	Sequence 518, App
17	117.5	4.7	1854	14	US-11-143-401-103	Sequence 103, App
18	117.5	4.7	1857	14	US-11-052-554A-534	Sequence 534, App
19	117	4.7	2656	11	US-11-088-306-13	Sequence 13, Appl
20	115.5	4.6	3051	14	US-11-103-957-42	Sequence 42, Appl
21	115	4.6	2087	11	US-11-072-512-84	Sequence 84, Appl
22	115	4.6	4139	7	US-10-204-639-98	Sequence 98, Appl
23	115	4.6	9903	14	US-11-052-554A-517	Sequence 517, App
c 24	115	4.6	37507	8	US-10-522-037-2	Sequence 2, Appli
25	114	4.6	1650	14	US-11-085-185-1	Sequence 1, Appli
26	114	4.6	1855	8	US-10-893-584-86	Sequence 86, Appl
27	114	4.6	8689	14	US-11-136-527-2554	Sequence 2554, Ap
28	113	4.5	1053	8	US-10-517-939-175	Sequence 175, App
29	113	4.5	1053	8	US-10-517-939-191	Sequence 191, App
30	111.5	4.5	5304	11	US-11-089-508-3	Sequence 3, Appli
31	111.5	4.5	5304	14	US-11-052-554A-751	Sequence 751, App
32	110	4.4	2712	9	US-10-932-182A-174038	Sequence 174038,
33	110	4.4	2712	9	US-10-932-182A-174038	Sequence 174038,
34	109	4.4	1375	14	US-11-108-163B-1	Sequence 1, Appli
35	109	4.4	4911	9	US-10-932-182A-75783	Sequence 75783, A
36	109	4.4	4911	9	US-10-932-182A-75783	Sequence 75783, A
37	108.5	4.4	3024	8	US-10-517-939-83	Sequence 83, Appl
38	107.5	4.3	3975	11	US-11-089-508-11	Sequence 11, Appl
39	107	4.3	986	11	US-11-096-568A-19160	Sequence 19160, A
40	107	4.3	1065	8	US-10-517-939-215	Sequence 215, App
41	106.5	4.3	8709	14	US-11-052-554A-475	Sequence 475, App
42	106	4.3	2460	9	US-10-932-182A-174454	Sequence 174454,
43	106	4.3	2460	9	US-10-932-182A-174454	Sequence 174454,
44	106	4.3	4932	14	US-11-052-554A-555	Sequence 555, App
45	105.5	4.2	9585	14	US-11-052-554A-474	Sequence 474, App

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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:37:30 ; Search time 40 Seconds
(without alignments)
1120.925 Million cell updates/sec

Title: US-09-806-413A-8
Perfect score: 2490
Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLPSA 466

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1547.5	62.1	480	2	JC7866	endo-1,6-beta-D-gl
2	517	20.8	469	2	A87467	glycosyl hydrolase
3	397	15.9	508	2	T34017	hypothetical prote
4	386	15.5	561	2	T31965	hypothetical prote
5	358.5	14.4	515	1	A32931	glucosylceramidase
6	340.5	13.7	566	2	T31964	hypothetical prote
7	320	12.9	536	1	EUHUGC	glucosylceramidase
8	289	11.6	522	2	T18583	glucosylceramidase
9	232	9.3	462	2	T17480	endo-xylanase homo
10	205	8.2	422	2	E69892	endo-xylanase homo
11	162.5	6.5	263	4	I67792	probable glucosylc
12	147	5.9	1054	2	T30933	chitinase (EC 3.2.
13	137	5.5	3705	2	AD0123	probable autotrans
14	134.5	5.4	669	2	I54205	galactosylceramida
15	132.5	5.3	943	2	T35497	hypothetical prote
16	132.5	5.3	5291	2	F90696	hypothetical prote
17	131.5	5.3	5188	2	B85547	probable RTX famil
18	130	5.2	997	2	I39739	mannuronan C5 epim

19	130	5.2	2554	2	AB3528	extracellular seri
20	128.5	5.2	1217	2	S52714	sericin1B - silkwo
21	128	5.1	1275	2	T33369	hypothetical prote
22	126	5.1	1286	2	S28634	adhesin AIDA-I pre
23	126	5.1	2334	2	S32920	cell wall-associat
24	126	5.1	3624	2	AD0835	large repetitive p
25	126	5.1	4199	2	S76412	hypothetical prote
26	124.5	5.0	3029	2	S76109	hypothetical prote
27	124	5.0	2817	2	B97033	uncharacterized pr
28	123	4.9	583	2	F69153	conserved hypothet
29	123	4.9	1742	2	S76110	hypothetical prote
30	122.5	4.9	918	2	T02759	hypothetical prote
31	122	4.9	335	2	T50601	endo-1,4-beta-xyla
32	122	4.9	2348	2	AD1841	hypothetical prote
33	121.5	4.9	635	2	S57714	cspB protein - Clo
34	121.5	4.9	786	2	T16509	hypothetical prote
35	121.5	4.9	1196	2	A29130	beta-amylase (EC 3
36	121	4.9	333	1	JS0590	endo-1,4-beta-xyla
37	121	4.9	1026	2	A48995	paracrystalline su
38	121	4.9	1073	2	C87374	S-layer protein Rs
39	121	4.9	3083	2	AH2493	hypothetical prote
40	120	4.8	3016	2	S77300	hypothetical prote
41	119.5	4.8	728	2	A75582	serine proteinase,
42	119.5	4.8	993	2	AE1905	outer membrane sec
43	119	4.8	1461	2	E90696	hypothetical prote
44	119	4.8	1461	2	A85547	hypothetical prote
45	118.5	4.8	1006	2	T31685	beta-galactosidase

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 7, 2006, 12:25:10 ; Search time 3728 Seconds
(without alignments)
5848.385 Million cell updates/sec

Title: US-09-806-413A-8
Perfect score: 2490
Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLPSA 466

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/abss/ABSSWEB_spool/US09806413/runat_07042006_132432_29821/app_query.fasta_1
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss06h
-USER=US09806413@CGN_1_1_4015@runat_07042006_132432_29821 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%		Query		DB		ID		Description	
No.	Score	Match	Length							
1	495	19.9	518	2	BG279868				BG279868	b7a10np.r
2	359.5	14.4	1782	4	AK082767				AK082767	Mus muscu
3	326	13.1	2391	4	CR859809				CR859809	Pongo pyg
4	323	13.0	1732	4	CR610547				CR610547	full-leng
5	323	13.0	1746	4	CR618224				CR618224	full-leng
6	323	13.0	1795	4	CR596605				CR596605	full-leng
7	323	13.0	1825	4	CR616044				CR616044	full-leng
8	323	13.0	1864	4	CR609535				CR609535	full-leng
9	322.5	13.0	2288	4	CR858547				CR858547	Pongo pyg
10	276.5	11.1	771	8	DR029374				DR029374	bda010074
11	276.5	11.1	777	8	DR032259				DR032259	bda020260
12	268	10.8	1505	11	DQ031033				DQ031033	Homo sapi
13	267	10.7	1255	8	DN687702				DN687702	CGX54-E12
14	266.5	10.7	1244	8	DN734894				DN734894	CNB78-C06
c 15	261.5	10.5	414	1	AJ517755				AJ517755	AJ517755
c 16	260	10.4	738	5	BW439330				BW439330	BW439330
17	260	10.4	826	8	CX206149				CX206149	MNS10221
18	243	9.8	630	5	BW517311				BW517311	BW517311
19	241.5	9.7	741	8	DR029733				DR029733	bda010084
20	241.5	9.7	1376	8	DN664890				DN664890	CFW22-G08
c 21	233.5	9.4	1044	5	BX398590				BX398590	BX398590
c 22	231.5	9.3	701	5	BW443131				BW443131	BW443131
23	231.5	9.3	761	5	BW482284				BW482284	BW482284
c 24	230	9.2	689	5	BW263737				BW263737	BW263737
25	224	9.0	893	8	DR438843				DR438843	EST149_38
26	223	9.0	892	8	DR438844				DR438844	EST149_36
27	221	8.9	818	7	CJ018053				CJ018053	CJ018053
28	219	8.8	636	3	BI506528				BI506528	BB170027B
29	218.5	8.8	656	5	BW368261				BW368261	BW368261
30	217.5	8.7	896	5	BQ683460				BQ683460	AGENCOURT
31	216.5	8.7	806	8	DR438838				DR438838	EST149_27
32	214	8.6	762	7	CJ019353				CJ019353	CJ019353
33	213	8.6	633	7	CO058468				CO058468	Lr_PAHCF_
34	211.5	8.5	679	1	AA198668				AA198668	mul5a06.r
35	210.5	8.5	839	7	CO567854				CO567854	AGENCOURT
36	209	8.4	1120	8	DN727172				DN727172	CNB34-D11
37	209	8.4	1939	4	CR606706				CR606706	full-leng
c 38	207	8.3	749	3	BJ787330				BJ787330	BJ787330
c 39	207	8.3	779	3	BJ130384				BJ130384	BJ130384
40	207	8.3	923	5	BQ680695				BQ680695	AGENCOURT
41	206.5	8.3	930	3	BI697593				BI697593	603348762
42	205	8.2	733	8	DR440367				DR440367	EST149_02
43	205	8.2	900	5	BU185544				BU185544	AGENCOURT
c 44	204.5	8.2	766	3	BJ813849				BJ813849	BJ813849
45	204.5	8.2	879	8	CX967271				CX967271	JGI_CAAP2

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OM protein - protein search, using sw model

Run on: April 7, 2006, 13:34:12 ; Search time 233 Seconds
(without alignments)
1411.057 Million cell updates/sec

Title: US-09-806-413A-8
Perfect score: 2490
Sequence: 1 AASASAYCSNSAGNYKLSSI.....QKWSGNAPSQSVTTWVLPSA 466

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2490	100.0	488	2	Q4WBR2_ASPFU	Q4wbr2 aspergillus
2	1877	75.4	490	2	Q8J0I9_TRIHA	Q8j0i9 trichoderma
3	1544.5	62.0	480	1	NEG1_NEUCR	Q7m4t0 neurospora
4	1206	48.4	1040	2	Q52AA8_MAGGR	Q52aa8 magnaporthe
5	1189.5	47.8	452	2	Q8WZM6_TRIHA	Q8wzm6 trichoderma
6	550	22.1	647	2	Q82JP5_STRAW	Q82jp5 streptomyce
7	517	20.8	469	2	Q9A7G6_CAUCR	Q9a7g6 caulobacter
8	493.5	19.8	496	2	Q8A2J3_BACTN	Q8a2j3 bacteroides
9	401.5	16.1	636	2	Q8R5P9_THETN	Q8r5p9 thermoanaer
10	397	15.9	519	2	Q9UB00_CAEEL	Q9ub00 caenorhabdi
11	386	15.5	561	2	O16581_CAEEL	O16581 caenorhabdi
12	379.5	15.2	519	2	Q60UJ1_CAEER	Q60uj1 caenorhabdi
13	368	14.8	524	2	Q611J0_CAEER	Q611j0 caenorhabdi
14	367.5	14.8	443	2	Q8R5Q0_THETN	Q8r5q0 thermoanaer
15	365	14.7	523	2	O16580_CAEEL	O16580 caenorhabdi
16	358.5	14.4	515	1	GLCM_MOUSE	P17439 mus musculu
17	358.5	14.4	515	2	Q78NR7_MOUSE	Q78nr7 mus musculu
18	341.5	13.7	602	2	Q4P6A6_USTMA	Q4p6a6 ustilago ma
19	341	13.7	536	2	Q70KH2_PIG	Q70kh2 sus scrofa
20	340	13.7	439	2	Q4URV7_XANCP	Q4urv7 xanthomonas

21	336	13.5	548	2	Q8PBP2_XANCP	Q8pbp2	xanthomonas
22	331.5	13.3	495	2	Q611J5_CAEBR	Q611j5	caenorhabdi
23	328	13.2	458	2	Q8PN97_XANAC	Q8pn97	xanthomonas
24	326	13.1	536	2	Q5R8E3_PONPY	Q5r8e3	pongo pygma
25	323	13.0	536	1	GLCM_HUMAN	P04062	homo sapien
26	323	13.0	536	1	GLCM_PANTR	Q9bdt0	pan troglod
27	323	13.0	536	2	Q4VX22_HUMAN	Q4vx22	homo sapien
28	322.5	13.0	536	2	Q5RBT6_PONPY	Q5rbt6	pongo pygma
29	321	12.9	447	2	Q9KIJ7_SALTY	Q9kij7	salmonella
30	318.5	12.8	572	2	Q9AT27_PHYIN	Q9at27	phytophthor
31	316	12.7	575	2	Q4RID9_TETNG	Q4rid9	tetraodon n
32	309	12.4	520	2	Q628D0_CAEBR	Q628d0	caenorhabdi
33	297.5	11.9	667	2	Q4P3U0_USTMA	Q4p3u0	ustilago ma
34	290.5	11.7	437	2	Q7N4Q0_PHOLL	Q7n4q0	photorhabdu
35	289	11.6	522	2	Q9XTB0_CAEL	Q9xtb0	caenorhabdi
36	288	11.6	522	2	Q9BH43_CAEL	Q9bh43	caenorhabdi
37	265.5	10.7	551	2	Q8IMY3_DROME	Q8imy3	drosophila
38	265.5	10.7	573	2	Q4V4F5_DROME	Q4v4f5	drosophila
39	265.5	10.7	577	2	Q4V4J1_DROME	Q4v4j1	drosophila
40	264.5	10.6	561	2	Q9VCJ4_DROME	Q9vcj4	drosophila
41	254	10.2	506	2	Q7PXX9_ANOGA	Q7pxx9	anopheles g
42	249	10.0	458	2	Q8MQ76_CAEL	Q8mq76	caenorhabdi
43	232	9.3	462	2	O52801_AMYOR	O52801	amycolatops
44	223	9.0	424	2	Q4V4A3_DROME	Q4v4a3	drosophila
45	218.5	8.8	413	2	Q46961_ERWCH	Q46961	erwinia chr

SP. NT
Search Strategy for 09/806,413

(FILE 'HOME' ENTERED AT 10:24:22 ON 18 APR 2006)

FILE 'REGISTRY' ENTERED AT 10:24:43 ON 18 APR 2006

L1 2 S 3.2.1.58
L2 1 S 3.2.1.75
E "BETA-1,3-GLUCANASE"/CN 25
L3 0 S 3.2.1.149
E "PRIMEVEROSIDASE"/CN 25
L4 1 S E3

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
10:29:01 ON 18 APR 2006

L5 21663 S L2 OR L4 OR (BETA-1,3-GLUCANASE)
L6 114 S L5 AND FUMIGATUS
L7 81 DUP REM L6 (33 DUPLICATES REMOVED)
L8 86587 S (40 OR 41 OR 42 OR 43 OR 44 OR 45 OR 46 OR 47 OR 48 OR 49 OR
L9 3 S L8 AND L7
L10 1 S L7 AND AP-20
L11 7391 S (40,000 OR 41,000 OR 42,000 OR 43,000 OR 44,000 OR 45,000 OR
L12 14 S L11 AND FUMIGATUS
L13 0 S L12 AND L5

=>

SPNT
Search Strategy for 09/806,413

(FILE 'HOME' ENTERED AT 12:16:46 ON 18 APR 2006)

FILE 'REGISTRY' ENTERED AT 12:16:56 ON 18 APR 2006
E "PRIMEVEROSIDASE"/CN 25

L1 1 S E3
L2 1 S 9001-22-3

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
12:18:34 ON 18 APR 2006

L3 99 S (L1 OR L2) AND FUMIGATUS
L4 73 DUP REM L3 (26 DUPLICATES REMOVED)
L5 99 S L1 AND FUMIGATUS
L6 69 S PRIMEVEROSIDASE
L7 6 S L6 AND FUMIGATUS
L8 3 DUP REM L7 (3 DUPLICATES REMOVED)

=>



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- Search numbers may not be continuous; all searches are represented.
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Search	Most Recent Queries	Time	Result
#15	Search #12 AND fumigatus Limits: Publication Date to 1999	10:12:17	20
#14	Search #12 AND fumigatus	09:39:17	32
#13	Search #12 AND (aspergillus or fumigatus)	09:39:07	91
#12	Related Articles for PubMed (Select 12036053)	09:38:03	255
#11	Search #9 AND #6	09:32:36	1
#9	Search "b-primeverosidase protein, plant"[Substance Name]	09:32:10	4
#7	Search #2 AND #6	09:31:38	0
#6	Search "Aspergillus fumigatus"[MeSH]	09:31:26	3523
#4	Search #2 AND aspergillus	09:31:08	0
#3	Search #2 AND fumigatus	09:30:59	0
#2	Search "endo-1,6-beta-glucanase"[Substance Name]	09:30:39	33

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Apr 10 2006 06:29:53

SPN

EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	4580	glucanase or primeverosidase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/18 10:21
L2	145	I1 and fumigatus	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/18 10:16
L3	61	1,6-glucanase or 1,6glucanase or ("1, 6" adj glucanase)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/18 10:16
L4	9	I3 and I2	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/18 10:17
L5	15	primeverosidase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/18 10:21
L6	1	I5 and fumigatus	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/18 10:21
S1	0	rutinosidase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2006/04/18 10:15
S2	11	diglycosidase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/01/08 12:18
S3	9	primeverosidase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/01/08 12:19
S4	0	"3.2.1.149!"	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/01/08 12:19
S5	245918	yamamoto.in. or okada.in. or usui.in. or sakata.in. or toumoto.in. or tsuruhami.in.	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/01/08 12:20

SPM

EAST Search History

S6	16	(yamamoto.in. or okada.in. or usui.in. or sakata.in. or toumoto.in. or tsuruhami.in.) and (diglycosidase or primeverosidase)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2004/01/08 12:20
S7	331	(glucosidase or glycoside) near10 (aspergillus or penicillium or rhizomucor or corynebacterium or rhizopus or talaromyces or mortierella or cryptococcus or microbacterium or actinoplanes)	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/05/10 12:53
S8	0	S7 and primeverosidase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/05/10 12:55
S9	11	primeverosidase	US-PGPUB; USPAT; EPO; JPO; DERWENT	OR	OFF	2005/05/10 12:55